

SEQUENCE LISTING

<110> Martin, Gregory B.
Abramovitch, Robert B.
Lin, Nai-Chun
Kim, Young-Jin

<120> BACTERIAL EFFECTOR PROTEINS WHICH INHIBIT PROGRAMMED
CELL DEATH

<130> 3213/104

<140> 10/524,750

<141> 2003-08-13

<150> 60/404,339

<151> 2002-08-16

<150> 60/425,842

<151> 2002-11-12

<150> PCT/US03/25247

<151> 2003-08-16

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<170> PatentIn Ver. 2.1

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<211> 1662

<212> DNA

<213> Pseudomonas syringae

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<213> *Pseudomonas syringae*

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<212> PRT

<213> *Pseudomonas syringae*

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Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro
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Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala
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Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala
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Ile Val Pro

<210> 5

<211> 1740

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<213> Pseudomonas syringae

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 <213> *Pseudomonas syringae*

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gtcagggaga ctgttgccgc ctttgtaaac aaccgttacg agcggcaggc ggttggtgcc 1380
gacatacgcg cagccctaaa tttatctaaa caattcaata agttgcgtac ggtctctaag 1440
gccgatgctg cctccaataa accgggcttc aaggatctgg cggaccaccc agacgacgcg 1500
acgcaatgcc tttttggtga agaattgtcg ctgaccagtt cggttcagca ggtgatcggc 1560
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ctggcaggta aggcaacgga catgtcggag tcttacagcc gagaggcaaa taaggacctg 1620
 gtgttcatgg atatgaaaaa acttgcccaa ttcctcgag gcaagcctga gcatccgatg 1680
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<210> 8

<211> 579

<212> PRT

<213> *Pseudomonas syringae*

<400> 8

Met Ala Gly Ile Asn Gly Ala Gly Pro Ser Gly Ala Tyr Phe Val Gly
 1 5 10 15

His Thr Asp Pro Glu Pro Ala Ser Gly Gly Ala His Gly Ser Ser Ser
 20 25 30

Gly Ala Ser Ser Ser Asn Ser Pro Arg Leu Pro Ala Pro Pro Asp Ala
 35 40 45

Pro Ala Ser Gln Ala Arg Asp Arg Arg Glu Met Leu Leu Arg Ala Arg
 50 55 60

Pro Leu Ser Arg Gln Thr Arg Glu Trp Val Ala Gln Gly Met Pro Pro
 65 70 75 80

Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala
 85 90 95

Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp
 100 105 110

Ala Ala Ala Ser His Val Arg Thr Glu Gly Gly Arg Thr Pro Gln Ala
 115 120 125

Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn
 130 135 140

Arg Ile Val Gln Gln Leu Val Asp Ala Gly Ala Asp Leu Ala Gly Ile
 145 150 155 160

Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro
 165 170 175

Ser Arg Thr Val Gln Ser Ile Leu Ile Glu His Phe Pro His Leu Leu
 180 185 190

Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala

195		200		205
Ala Leu Arg Arg Glu Val Arg Gln Gln Glu Ala Ser Ala Pro Pro Arg				
210		215		220
Thr Ala Ala Arg Ser Ser Val Arg Thr Pro Glu Arg Ser Thr Val Pro				
225		230		235 240
Pro Thr Ser Thr Glu Ser Ser Ser Gly Ser Asn Gln Arg Thr Leu Leu				
		245		250 255
Gly Arg Phe Ala Gly Leu Met Thr Pro Asn Gln Arg Arg Pro Ser Ser				
		260		265 270
Ala Ser Asn Ala Ser Ala Ser Gln Arg Pro Val Asp Arg Ser Pro Pro				
		275		280 285
Arg Val Asn Gln Val Pro Thr Gly Ala Asn Arg Val Val Met Arg Asn				
		290		295 300
His Gly Asn Asn Glu Ala Asp Ala Ala Leu Gln Gly Leu Ala Gln Gln				
305		310		315 320
Gly Val Asp Met Glu Asp Leu Arg Ala Ala Leu Glu Arg His Ile Leu				
		325		330 335
His Arg Arg Pro Ile Pro Met Asp Ile Ala Tyr Ala Leu Gln Gly Val				
		340		345 350
Gly Ile Ala Pro Ser Ile Asp Thr Gly Glu Ser Leu Met Glu Asn Pro				
		355		360 365
Leu Met Asn Leu Ser Val Ala Leu His Arg Ala Leu Gly Pro Arg Pro				
		370		375 380
Ala Arg Ala Gln Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr				
385		390		395 400
Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile				
		405		410 415
Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu				
		420		425 430
Leu Ser Leu Asn Pro Gly Ala Gly Val Arg Glu Thr Val Ala Ala Phe				
		435		440 445
Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala				

450

455

460

Ala Leu Asn Leu Ser Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys
 465 470 475 480

Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Leu Ala Asp His
 485 490 495

Pro Asp Asp Ala Thr Gln Cys Leu Phe Gly Glu Glu Leu Ser Leu Thr
 500 505 510

Ser Ser Val Gln Gln Val Ile Gly Leu Ala Gly Lys Ala Thr Asp Met
 515 520 525

Ser Glu Ser Tyr Ser Arg Glu Ala Asn Lys Asp Leu Val Phe Met Asp
 530 535 540

Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu His Pro Met
 545 550 555 560

Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr Ala Phe Arg
 565 570 575

Ile Val Pro

<210> 9

<211> 16

<212> PRT

<213> *Pseudomonas syringae*

<400> 9

Ala Gly Pro Ser Gly Ala Tyr Phe Val Gly His Thr Asp Pro Glu Pro
 1 5 10 15

<210> 10

<211> 9

<212> PRT

<213> *Pseudomonas syringae*

<400> 10

Ser Gly Ala Ser Ser Ser Asn Ser Pro
 1 5

<210> 11

<211> 8
<212> PRT
<213> *Pseudomonas syringae*

<400> 11
Leu Ser Arg Gln Thr Arg Glu Trp
1 5

<210> 12
<211> 6
<212> PRT
<213> *Pseudomonas syringae*

<400> 12
Ile Val Gln Gln Leu Val
1 5

<210> 13
<211> 5
<212> PRT
<213> *Pseudomonas syringae*

<400> 13
Ser Ser Ser Gly Ser
1 5

<210> 14
<211> 11
<212> PRT
<213> *Pseudomonas syringae*

<400> 14
Pro Val Asp Arg Ser Pro Pro Arg Val Asn Gln
1 5 10

<210> 15
<211> 12
<212> PRT
<213> *Pseudomonas syringae*

<400> 15
Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr
1 5 10

<210> 16
<211> 5
<212> PRT
<213> Pseudomonas syringae

<400> 16
Ser Arg Arg Pro Asp
1 5

<210> 17
<211> 5
<212> PRT
<213> Pseudomonas syringae

<400> 17
Arg Ala Thr Arg Leu
1 5

<210> 18
<211> 15
<212> PRT
<213> Pseudomonas syringae

<400> 18
Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu Leu
1 5 10 15

<210> 19
<211> 5
<212> PRT
<213> Pseudomonas syringae

<400> 19
Val Ala Ala Phe Val
1 5

<210> 20
<211> 5
<212> PRT
<213> Pseudomonas syringae

<400> 20
Ile Arg Ala Ala Leu

1

5

<210> 21

<211> 5

<212> PRT

<213> *Pseudomonas syringae*

<400> 21

Ser Lys Ala Asp Ala

1

5

<210> 22

<211> 8

<212> PRT

<213> *Pseudomonas syringae*

<400> 22

Gln Gln Val Ile Gly Leu Ala Gly

1

5

<210> 23

<211> 38

<212> PRT

<213> *Pseudomonas syringae*

<400> 23

Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu

1

5

10

15

His Pro Met Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr

20

25

30

Ala Phe Arg Ile Val Pro

35

<210> 24

<211> 553

<212> PRT

<213> *Pseudomonas syringae*

<220>

<221> UNSURE

<222> (1)..(6)

<223> Xaa at positions 1-6 can be any amino acid

<220>
<221> UNSURE
<222> (23)..(31)
<223> Xaa at positions 23-31 can be any amino acid

<220>
<221> UNSURE
<222> (41)..(70)
<223> Xaa at positions 41-70 can be any amino acid

<220>
<221> UNSURE
<222> (79)..(131)
<223> Xaa at positions 79-131 can be any amino acid

<220>
<221> UNSURE
<222> (138)..(220)
<223> Xaa at positions 138-220 can be any amino acid

<220>
<221> UNSURE
<222> (226)..(253)
<223> Xaa at positions 226-253 can be any amino acid

<220>
<221> UNSURE
<222> (265)..(360)
<223> Xaa at positions 265-360 can be any amino acid

<220>
<221> UNSURE
<222> (373)
<223> Xaa at position 373 can be any amino acid

<220>
<221> UNSURE
<222> (379)..(380)
<223> Xaa at positions 379-380 can be any amino acid

<220>
<221> UNSURE
<222> (386)..(390)
<223> Xaa at positions 386-390 can be any amino acid

<220>
<221> UNSURE

<222> (406)..(433)
<223> Xaa at positions 406-433 can be any amino acid

<220>
<221> UNSURE
<222> (439)..(451)
<223> Xaa at positions 439-451 can be any amino acid

<220>
<221> UNSURE
<222> (457)..(489)
<223> Xaa at positions 457-489 can be any amino acid

<220>
<221> UNSURE
<222> (498)..(515)
<223> Xaa at positions 498-515 can be any amino acid

<400> 24
Xaa Xaa Xaa Xaa Xaa Xaa Ala Gly Pro Ser Gly Ala Tyr Phe Val Gly
1 5 10 15
His Thr Asp Pro Glu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser
20 25 30
Gly Ala Ser Ser Ser Asn Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Xaa Xaa Xaa Xaa Xaa Leu Ser Arg Gln Thr Arg Glu Trp Xaa Xaa
65 70 75 80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125
Xaa Xaa Xaa Ile Val Gln Gln Leu Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	165	170	175
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	180	185	190
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	195	200	205
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Ser	Ser	Gly		210	215	220
Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	225	230	235
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Val	Asp	245	250	255
Arg	Ser	Pro	Pro	Arg	Val	Asn	Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	260	265	270
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	275	280	285
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	290	295	300
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	305	310	315
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	325	330	335
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	340	345	350
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Pro	Arg	Pro	Ala	Val	Pro	Val		355	360	365
Ala	Pro	Ala	Thr	Xaa	Ser	Arg	Arg	Pro	Asp	Xaa	Xaa	Arg	Ala	Thr	Arg		370	375	380
Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Glu	Asp	Tyr	Glu	Asn	Asn	Val	Ala	Tyr		385	390	395
Gly	Val	Arg	Leu	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	405	410	415

Val Ala Ala Phe Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
420 425 430

Xaa Ile Arg Ala Ala Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445

Xaa Xaa Xaa Ser Lys Ala Asp Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
450 455 460

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
465 470 475 480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln Val Ile Gly Leu Ala
485 490 495

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
500 505 510

Xaa Xaa Xaa Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly
515 520 525

Lys Pro Glu His Pro Met Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile
530 535 540

Ala Lys Tyr Ala Phe Arg Ile Val Pro
545 550

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

gtaatgcagc gcctccctat c

21

<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 26
tcaggggact attctaaaag c 21

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 27
atggcgggta tcaatagagc g 21

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 28
tcacacccgc aatcgtgttg cac 23

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
tcatacatgt ctttcaaggc ccg 23

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
gtatcaatag agcgggacca tc 22

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
cactgaccac ttgctgaacg 20

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
tgtcgcgcca aaccagggcg tg 22

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
ccatcaccag ggcaaacc 18

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
gtatcgttca gcaattggtc agtg 24

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
acgcgtatgg gtcttttggtt g 21

<210> 36
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 36
acgattgcgg gtgatgc 17

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 37
cctcttggct gtaaggctgc 20

<210> 38
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
atggcgggta tcaatagagc gg 22

<210> 39
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
gaattcgata tcaagcttat cgataccgtc gacctcgag 39

<210> 40
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
gaattcgaat tgggatatca agcttatcga taccgtcgac ctcgag 46

<210> 41
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
gaattcgaat tgatatcaag cttatcgata ccgtcgacct cgag 44

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
cggaggcgaa cagccgagca g 21

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
gcaattcgaa gtggcagtga 20

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
ttatgcttta ttggtatttt tagagg 26

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
atggcgggta tcaatagagc 20

<210> 46
<211> 26
<212> DNA
<213> Pseudomonas syringae

<220>
<221> unsure

<222> (7)..(22)

<223> N at positions 7-22 can be A, C, T, or G

<400> 46

ggaactnnnn nnnnnnnnnn nccac

26

<210> 47

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 47

Met Ala Gly Ile Asn Arg Ala Gly

1

5

<210> 48

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<221> UNSURE

<222> (2)

<223> Xaa at position 2 can be any amino acid except E

<220>

<221> UNSURE

<222> (3)

<223> Xaa at position 3 can be any amino acid except D

<220>

<221> UNSURE

<222> (4)

<223> Xaa at position 4 can be any amino acid except R

<220>

<221> UNSURE

<222> (5)

<223> Xaa at position 5 can be any amino acid except K

<220>
<221> UNSURE
<222> (6)
<223> Xaa at position 6 can be any amino acid except H

<220>
<221> UNSURE
<222> (7)
<223> Xaa at position 7 can be any amino acid except P

<220>
<221> UNSURE
<222> (8)
<223> Xaa at position 8 can be any amino acid except F

<220>
<221> UNSURE
<222> (9)
<223> Xaa at position 9 can be any amino acid except Y

<220>
<221> UNSURE
<222> (10)
<223> Xaa at position 10 can be any amino acid except W

<220>
<221> UNSURE
<222> (11)..(12)
<223> Xaa at positions 11-12 can be any amino acid

<220>
<221> UNSURE
<222> (19)
<223> Xaa at position 19 can be any amino acid except P

<400> 48
Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Thr Ala Gly
1 5 10 15

Cys Asn Xaa

<210> 49
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence

<220>
<221> UNSURE
<222> (2)..(3)
<223> Xaa at positions 2-3 can be any amino acid

<220>
<221> UNSURE
<222> (5)..(6)
<223> Xaa at positions 5-6 can be any amino acid

<220>
<221> UNSURE
<222> (8)..(9)
<223> Xaa at positions 8-9 can be any amino acid

<220>
<221> UNSURE
<222> (11)
<223> Xaa at position 11 can be any amino acid

<220>
<221> UNSURE
<222> (13)..(15)
<223> Xaa at positions 13-15 can be any amino acid

<400> 49
Arg Xaa Xaa Leu Xaa Xaa Ser Xaa Xaa Leu Xaa Arg Xaa Xaa Xaa Glu
1 5 10 15

<210> 50
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 can be any amino acid

<220>
<221> UNSURE
<222> (4)
<223> Xaa at position 4 can be any amino acid

<400> 50
Ser Xaa Arg Xaa Arg
1 5

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence

<220>
<221> UNSURE
<222> (4)..(8)
<223> Xaa at positions 4-8 can be any amino acid

<400> 51
Asn Pro Ser Xaa Xaa Xaa Xaa Xaa Ser
1 5

<210> 52
<211> 539
<212> PRT
<213> Pseudomonas syringae

<400> 52
Met Pro Gly Ile Asn Gly Ala Gly Pro Ser Asn Phe Phe Trp Gln Trp
1 5 10 15

Arg Thr Asp Gly Glu Pro Val Thr Glu Arg Glu His Asp Ser Ser Arg
20 25 30

Ser Ala Ser Ser Ala Asn Ser Pro Glu Leu Pro Pro Pro Ala Ser Pro
35 40 45

Ala Glu Ser Gly Arg Gln Arg Leu Leu Arg Ser Ser Ala Leu Ser Arg
50 55 60

Gln	Thr	Arg	Glu	Trp	Leu	Glu	Ala	Thr	Pro	Ala	Arg	Val	Gln	Gly	Ala	
65					70					75					80	
Thr	Pro	Pro	Ala	Glu	Ala	Arg	Gln	Ser	Pro	Glu	Ala	Gln	Gln	Ala	Glu	
				85					90					95		
Arg	Ile	Val	Gln	Glu	Leu	Val	Arg	Gly	Gly	Ala	Asp	Leu	Asn	Asn	Val	
			100					105					110			
Arg	Thr	Met	Leu	Arg	Asn	Val	Met	Asp	Asn	Asn	Ala	Val	Ala	Phe	Ser	
		115					120					125				
Arg	Val	Glu	Arg	Asp	Ile	Leu	Leu	Gln	His	Phe	Pro	Asn	Met	Pro	Met	
	130					135					140					
Thr	Gly	Ile	Ser	Ser	Asp	Ser	Val	Leu	Ala	Asn	Glu	Leu	Arg	Gln	Arg	
145					150					155					160	
Leu	Arg	Gln	Thr	Val	Arg	Gln	Gln	Arg	Ile	Gln	Ser	Ser	Thr	Pro	Ala	
				165					170					175		
Arg	Leu	Ala	Asp	Ser	Ser	Ser	Gly	Ser	Ser	Gln	Arg	Ser	Leu	Ile	Gly	
			180					185					190			
Arg	Ser	Thr	Met	Leu	Met	Thr	Pro	Gly	Arg	Ser	Ser	Ser	Ser	Ser	Ala	
		195					200					205				
Ala	Ala	Ser	Arg	Thr	Ser	Val	Asp	Arg	His	Pro	Gln	Gly	Leu	Asp	Leu	
	210					215					220					
Glu	Ser	Ala	Arg	Leu	Ala	Ser	Ala	Ala	Arg	His	Asn	His	Ser	Ala	Asn	
225					230					235					240	
Gln	Thr	Asn	Glu	Ala	Leu	Arg	Arg	Leu	Thr	Gln	Glu	Gly	Val	Asp	Met	
				245					250					255		
Glu	Arg	Leu	Arg	Thr	Ser	Leu	Gly	Arg	Tyr	Ile	Met	Ser	Leu	Glu	Pro	
			260					265					270			
Leu	Pro	Pro	Asp	Leu	Arg	Arg	Ala	Leu	Glu	Ser	Val	Gly	Ile	Asn	Pro	
		275					280					285				
Phe	Ile	Pro	Glu	Glu	Leu	Ser	Leu	Val	Asp	His	Pro	Val	Leu	Asn	Phe	
	290					295					300					
Ser	Ala	Ala	Leu	Asn	Arg	Met	Leu	Ala	Ser	Arg	Gln	Thr	Thr	Thr	Asn	
305					310					315					320	

Ser Pro Glu Leu Pro Pro Leu Ala Ser Ser Ala Glu Ser Gly Arg Arg
 325 330 335
 Arg Leu Leu Arg Ser Pro Pro Leu Leu Ser Gly Gln Arg Glu Trp Ile
 340 345 350
 Glu Gln Ser Met Arg Gln Glu Ala Glu Pro Gln Ser Ser Arg Leu Asn
 355 360 365
 Arg Ala Val Arg Leu Ala Val Met Pro Pro Gln Asn Glu Asn Glu Asp
 370 375 380
 Asn Val Ala Tyr Ala Ile Arg Leu Arg Arg Leu Asn Pro Gly Ala Asp
 385 390 395 400
 Val Ser Arg Val Val Ala Ser Phe Ile Thr Asp Pro Ala Ala Arg Gln
 405 410 415
 Gln Val Val Asn Asp Ile Arg Ala Ala Leu Asp Ile Ala Pro Gln Phe
 420 425 430
 Ser Gln Leu Arg Thr Ile Ser Lys Ala Asp Ala Glu Ser Glu Glu Leu
 435 440 445
 Gly Phe Arg Asp Ala Ala Asp His Pro Asp Asn Ala Thr Ser Cys Leu
 450 455 460
 Phe Gly Glu Glu Leu Ser Leu Ser Asn Pro Asp Gln Gln Val Ile Gly
 465 470 475 480
 Leu Ala Val Asn Pro Thr Asp Lys Pro Gln Pro Tyr Ser Gln Glu Val
 485 490 495
 Asn Lys Ala Leu Thr Phe Met Asp Met Lys Lys Leu Ala Gln Tyr Leu
 500 505 510
 Ala Asp Lys Pro Glu His Pro Leu Asn Arg Gln Arg Leu Asp Ala Lys
 515 520 525
 Asn Ile Ala Lys Tyr Ala Phe Lys Ile Val Pro
 530 535

<210> 53

<211> 158

<212> PRT

<213> Pseudomonas syringae

<400> 53

Met Gly Asn Ile Cys Val Gly Gly Ser Arg Met Ala His Gln Val Asn
1 5 10 15

Ser Pro Asp Arg Val Ser Asn Asn Ser Gly Asp Glu Asp Asn Val Thr
20 25 30

Ser Ser Gln Leu Leu Ser Val Arg His Gln Leu Ala Glu Ser Ala Gly
35 40 45

Leu Pro Arg Asp Gln His Glu Phe Val Ser Ser Gln Ala Pro Gln Ser
50 55 60

Leu Arg Asn Arg Tyr Asn Asn Leu Tyr Ser His Thr Gln Arg Thr Leu
65 70 75 80

Asp Met Ala Asp Met Gln His Arg Tyr Met Thr Gly Ala Ser Gly Ile
85 90 95

Asn Pro Gly Met Leu Pro His Glu Asn Val Asp Asp Met Arg Ser Ala
100 105 110

Ile Thr Asp Trp Ser Asp Met Arg Glu Ala Leu Gln His Ala Met Gly
115 120 125

Ile His Ala Asp Ile Pro Pro Ser Pro Glu Arg Phe Val Ala Thr Met
130 135 140

Asn Pro Ser Gly Ser Ile Arg Met Ser Thr Leu Ser Pro Ser
145 150 155

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<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<221> UNSURE

<222> (2)

<223> Xaa at position 2 can be any amino acid

<220>

<221> UNSURE

<222> (4)..(5)

<223> Xaa at positions 4-5 can be any amino acid

<220>

<221> UNSURE

<222> (7)..(8)

<223> Xaa at positions 7-8 can be any amino acid

<220>

<221> UNSURE

<222> (10)..(11)

<223> Xaa at positions 10-11 can be any amino acid

<220>

<221> UNSURE

<222> (13)

<223> Xaa at position 13 can be any amino acid

<220>

<221> UNSURE

<222> (15)..(17)

<223> Xaa at positions 15-17 can be any amino acid

<400> 54

Ser Xaa Arg Xaa Xaa Leu Xaa Xaa Ser Xaa Xaa Leu Xaa Arg Xaa Xaa
1 5 10 15

Xaa Glu